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Literature biases may cause island-restricted reptiles to lack research effort compared to their mainland counterparts

Abstract

Island species are disproportionately threatened by extinction compared to their mainland counterparts. Reptiles possess a vast amount of phylogenetic diversity but many are also threatened, meaning the potential loss of this diversity is high. This is exacerbated on islands as reptiles here often represent endemic radiations and contribute crucial services to the ecosystem such as seed dispersal and pollination. This study analysed over 89,000 research publications from 1960-2021 to compare the research output between island-restricted reptiles (IRRs) and mainland species. I investigated physiological, geographical, and socioeconomic characteristics of each species and the regions they reside in to determine how they affected IRR research. IRRs were substantially understudied compared to mainland reptiles, comprising only 7.2% of reptile research despite representing over 2,400 species (23% of all described species). While factors like body mass and threat status influenced research output similarly between the two groups, IRRs exhibited a negative relationship between range size and research output, contrasting with mainland species. Research output was significantly less in IRRs versus mainland species across certain biogeographic realms and IUCN threat categories. IRRs comprised 12 of the top 15 species identified as the highest priority for future research based on a metric accounting for research deficiency, threat status, and taxonomic distinctiveness. The identified paucity of research on IRRs is concerning given their elevated extinction risk and ecological importance on islands. Focused research targeting IRRs, especially threatened and data deficient species is crucial for informing evidence-based conservation of these understudied reptiles and the insular ecosystems they inhabit.

1. Introduction

With over 11,000 species, reptiles comprise one of the most species-rich terrestrial vertebrate groups (The Reptile Database, 2024). Due to their long evolutionary history reptiles have had time to speciate and adapt to an abundance of unique environments, allowing them to inhabit a wide variety of ecosystems. As a result of their rich variety, reptiles contribute greatly to the ecosystems they inhabit via means such as pollination, population control and ecosystem engineering (Doody et al., 2021; Esposito et al., 2021; Valencia-Aguilar et al., 2013). As well as variety in ecosystems, reptiles also inhabit a range of niches across many trophic levels, this helps them to contribute to the innate benefits of a biodiverse ecosystem such as protection from environmental perturbations (Hooper et

al., 2005). This niche diversity is reflected in the high functional and phylogenetic diversity of reptiles (Valencia-Aguilar et al., 2013) that let many species coexist allowing them to propagate and play key roles in energy flow and nutrient cycling (Valencia-Aguilar et al., 2013).

Despite their importance to the ecosystems they inhabit, a significant proportion of extant reptiles are under considerable threat of extinction from anthropogenic factors such as agriculture, logging, and invasive species (Sparling et al., 2010). The scope of which reptile species are at risk is so great that with the loss of just the currently threatened species, we could lose a cumulative 15.6 billion years of phylogenetic diversity (Cox et al., 2022), more than amphibians, birds, or mammals (Gumbs et al., 2020). With this loss, we will also lose their unique contributions to the ecosystems they reside in. The conservation of reptiles is therefore important but requires research in order to support evidence-based conservation efforts (Gumbs et al., 2020). Despite their significance, reptiles are still more data deficient than mammals (The Reptile Database, 2024). This can be detrimental to reptile conservation as studies on squamates show up to 21% of data deficient or not evaluated species may be threatened, this is three times the amount seen in assessed species (Wotherspoon et al., 2024). This highlights the need for a greater focus on reptile research as to protect these at-risk species.

Reptiles are important elements of many island ecosystems (de Miranda, 2017), contributing significantly to their biodiversity, for example by allowing plant communities to establish and diversify through seed dispersal and genetic exchange as a result of pollination (Esposito et al., 2021; Pérez-Méndez et al., 2016). Despite only making up around 6.7% of the Earth's surface area, islands are home to roughly 20% of the Earth's biodiversity (Fernández-Palacios et al., 2021). As some of the most successful island colonisers, reptiles are often highly abundant and relatively well-represented in island ecosystems (Ali & Meiri, 2019) making them valuable food sources for other insular species (Jesus et al., 2005). A good example of reptile diversity on islands is Madagascar, which is home to over 450 reptile species, roughly 3.8% of all known extant species (The Reptile Database, 2024). Other than reptile diversity the isolated nature of islands also creates distinctive abiotic conditions as well as unique intra and inter-species dynamics (Russell & Kueffer, 2019), facilitating speciation and leading to a high level of unique endemic species (Conenna et al., 2017). An example of this is the Tarentola geckos found in the Cape Verde archipelago. This group experienced rapid evolutionary radiation in the last 7.7 million years after they arrived from the Canary Islands and underwent multiple speciation events (Vasconcelos et al., 2012). To conclude, due to their outstanding ability to colonise and diversify on islands (Ali & Meiri, 2019), reptiles are important as they help to increase biodiversity in island ecosystems after their colonisation which helps other species to propagate.

However, island biodiversity, including that of reptiles, is currently in jeopardy due to a multitude of factors such as habitat loss, invasive species and wildlife trading (Chng et al., 2023; Reaser et al., 2007) Indeed, almost 90% of all historical reptile extinctions have been island species and around half of all threatened species are also found on islands (Fernández-Palacios et al., 2021). This is due to the high level of anthropogenic modification and the general scarcity of conservation efforts directed towards islands (Nori et al., 2022). In regard to reptiles, this loss may be in part due to the lack of studies and data which can be used to inform evidence-based conservation strategies (Gumbs et al., 2020). More knowledge is needed to understand the ecological roles and threats island reptiles face. Therefore, Increasing the number of studies focused on island reptiles can help produce higher-quality conservation strategies and outcomes (Sutherland et al., 2004) as well as increase the general awareness of the importance of island reptiles.

However, more studies do not always lead to more directed conservation action. In many cases, the number of studies on a taxon is not evenly distributed as some families or species may have a large amount of research directed at them whereas some may have none (Brooke et al., 2014). Therefore, identifying and addressing the causes for these gaps in the literature is vital for directing future research at the species that could benefit the most from it. The purpose of a knowledge gap analysis is to examine the existing literature on a subject, identify the trends that emerge, and uncover the underlying factors driving those patterns. Many knowledge gap analyses have been conducted in the past to identify the biases in the literature and direct the future conservation of other taxa such as primates (Chen et al., 2023), amphibians (Silva et al., 2020) and even some targeting reptiles at a global scale (Guedes et al., 2023). They have also been shown to be useful in understanding knowledge gaps in island-restricted species of specific groups such as bats and birds (Conenna et al., 2017; De Lima et al., 2011). However, none look specifically at island reptiles, to investigate the biases in research they face especially when compared to their mainland counterparts.

The goal of this project is to understand what affects the research output of Island-Restricted Reptile species (IRRs) and compare that with their mainland counterparts. During this study, I will investigate taxonomic, spatial and conservation status-related patterns associated with IRR research. I will also assess how certain physiological, geographical, and socioeconomic factors affect the research output of reptile species, and how this varies between IRRs and mainland reptile species. Additionally, I will also be ranking the reptile species most in need of research, based on their current research output, extinction risk and how taxonomically distinct they may be. I outline below the core questions that I address during this project:

1. When compared to mainland species, are IRRs understudied at an individual and family level? I predict that IRRs receive less research attention than their mainland counterparts at both the individual and family level, with relatively few species garnering the majority of the research effort targeting IRRs.

2. What are the key physiological, geographical, and socioeconomic factors affecting the research effort of IRRs and do they affect mainland reptiles in the same way? I predict variables such as range size will positively correlate with the research effort of IRRs and mainland reptiles however, this could still result in research gaps if IRRs have smaller ranges on average.

3. Which reptile species should be prioritised for future study? I anticipate IRRs will be represented far more frequently in the most high-ranking species when reptiles are ranked by their research need.

2. Methods

2.1 Defining Island Restricted Reptile Species

Reptile distribution data was obtained from Roll et al., (2017) and ArcGIS was used to exclude species with range occurrences on mainland areas (defined as any landmasses of sizes equal to or larger than Australia). Once IRRs had been identified, we could then categorise each different reptile species as either island-restricted or non-island-restricted (which we also refer to as mainland species).

2.2 Comparison of research outputs between island-restricted and mainland reptiles

The research outputs of the different reptile species (defined as the number of published scientific papers on that species) were obtained from Guedes et al., 2023. The database contained the total research output between 1960 and 2021 of all known reptile species, obtained by searching for a species' name and any of its synonyms in the Scopus database. If a paper was found with any of that species' known names in the title, abstract or keywords this was considered as one research output(Guedes et al. 2023.)

I compared research output between IRRs and mainland reptiles with a simple descriptive bibliometric analysis, allowing the mean number of papers at different taxonomic levels to be identified. With

taxonomic data sourced from Zheng & Wiens, 2016; Guedes et al., 2023; Phylogeny of Reptiles and Amphibians, 2024. I conducted analysis primarily at the species and family level with suborder also considered for specific analyses. At the species level, I identified the 10 most studied species and found how much research output was distributed across all reptile species. At the family level, I ranked the most studied families by the mean research output species in that family had. I also ranked the least studied families by the percentage of species in that family with no research outputs. This allowed me to investigate if IRRs were disproportionately represented at either extreme of families with the most or least research outputs. Finally, I compared the research output on IRRs at the suborder level to the number of threatened species (i.e., species classified as vulnerable, endangered, or critically endangered in the IUCN Red List) in that suborder to investigate how well represented each suborder is in the current scientific literature relative to how threatened it is.

2.3 Factors that affect research output in reptiles

I used General Linear Mixed Models (GLMMs) to investigate the physiological, geographical, and socioeconomic factors that affect the research for island-restricted and mainland species. I used separate analyses for IRRs and mainland reptiles to determine differences in the impact the covariables had on these two groups. Using eight covariables (not using biogeographic realm as it didn't fit this model) as fixed factors (Table 1), I ran separate global GLMMs on IRRs and then mainland reptile species, using a negative binomial distribution. Taxonomic family was included as a random effect to help account for the large amount of variation in research effort between families. To correct for skewness all data was log 10 transformed and the IUCN status was z-transformed to convert it from a categorical to an ordinal variable (Guedes et al., 2023). Finally, the dredge function from the MuMIn package in R was used to find which combination of covariables created a model that best explained the trends in the data.

I then investigated the effects of the individual biogeographic realms and IUCN statuses on research output using a Kruskal-Wallace rank sum test. I then conducted GLMMs followed by a multiple comparison test with Tukey contrasts using the R package multcomp to independently investigate if IRRs and mainland reptiles differed in the number of research outputs they had within each IUCN status and or biogeographic realm. Family was again used as the random effect, with the different models ran independently using the individual IUCN categories or biogeographic realms as the fixed effects. For this each species was categorised into its designated realm and IUCN category and if it was island-restricted or not (e.g. A species may be in the "Near threatened Island" and "Afrotropic Island categories").

Table 1. Description of the explanatory covariables used to investigate reptile research output.

COVARIABLE	TYPE	DESCRIPTION	SOURCE
YEAR OF DESCRIPTION	Discrete	The year the species was first described	Tonini et al., 2016
FAMILY / SUBORDER	Categorical	The taxonomic family / suborder the species is part of	Tonini et al., 2016
NUMBER OF BIOLOGICAL INSTITUTIONS	Discrete	The number of biological institutions in the range of the species	Guedes et al., 2023
RANGE SIZE (KM²)	Discrete	The range size of the species	Guedes et al., 2023
RANGE RARITY	Continuous	A measure of endemism and species richness of a species	Guedes et al., 2023
ELEVATION (M)	Continuous	Average elevation a species is found at	Guedes et al., 2023
BIOGEOGRAPHIC REALM	Categorical	What Biogeographic realm is the species found in	Guedes et al., 2023
THREAT STATUS	Ordinal	The IUCN threat status of the species[1]	IUCN, 2024
BODY MASS (G)	Continuous	The average body mass of a typical adult of the species	Colston et al., 2020; Feldman et al., 2016

[1] The threat status categories ranging from lowest risk of extinction to highest are as follows: Least Concern (LC), Near Threatened (NT), Vulnerable (VU), Endangered (EN), Critically Endangered (CR) Extinct in the Wild (EW), and Extinct (EX). Species with insufficient data to determine extinction risk are classified as Data Deficient (DD). A total of 1272 species that have not yet been categorised by IUCN were considered as Not Categorised (NC).

2.4 Research prioritisation

We identified the species of reptile most in need of study, using an index to quantify research need per species. This was done using a Research Prioritisation Metric (RPM) first defined by Roberts et al., 2016 and later refined by Conenna et al., 2017 to more accurately take into account species that were data deficient or not categorized by the IUCN Red List. This is necessary as data deficient species have been shown to be likely to have an unrecognised but high risk of extinction (Bland et al., 2015), and is

particularly relevant for this study as around half of data deficient reptiles may be threatened (Borgelt et al., 2022). The RPM is defined as follows:

RPM = ROi+ERi+0.5*CSi+0.5*ROCSi

The factors included are:

1. Research Output Index (ROi) - general research output index, obtained by dividing general research output (RO) by the maximum RO output recorded among IRRs, and subtracting it from 1. It ranges from 0 to 1, where 1 corresponds to species with no RO.
2. Extinction Risk Index (ERi) - ranging from 0 to 1, where 1 represents threatened species (vulnerable, endangered and critically endangered) and 0 non-threatened (least concern and near threatened). data deficient and not categorised IUCN species were accounted for by assigning a value of 1 when the species was a single-island endemic and the cumulative area of islands occupied was <400000 km^2, a value of 0.5 when only one of these conditions was verified and 0 when none of them.
3. Congeneric Species Index (CSi) - index of number of congeneric species, obtained by dividing the number of congeneric species (CS) by the maximum CS recorded among IRRs and subtracting it from 1. The index ranges from 0 to 1, 1 representing species with no recorded congenerics.
4. Research Output Congeneric Species index (ROCSi) - index of research output among CS. It was obtained by calculating total general RO among CS, and then dividing the value by the maximum total general RO among CS recorded, and finally subtracting it from 1. This index ranges from 0 to 1, where 1 represents no RO among CS.

The output RPM ranges between 0-3 with 3 identifying species that should be of the highest priority for research. This is due to them having low (or no) research outputs, being at greater threat of extinction and having a high taxonomic distinctiveness, This means they are species with a high risk of extinction, a lack of an evidence base on which to make conservation decisions, and if they were to go extinct would lead to a higher loss of evolutionary history. Further details about this metric can be found in Conenna et al 2017.

3. Results

3.1 Island-restricted reptiles have lower research output than mainland reptiles

3.1.1 Species-level patterns

Only 7.2% of the reptile-associated research outputs were devoted to IRRs (n = 6,401 papers across 2,438 species $vs.$ n = 82,879 papers across 8,094 species, for IRRs and non-IRRs, respectively). IRRs were substantially understudied compared to mainland species (2.7 ± 0.296 vs. 10.4 ± 0.714 papers per species for IRRs and non-IRRs, respectively; mean ± SE). Furthermore, nearly half (47.6%) of IRRs had no research outputs (vs 35.4% for non-IRRs)

The distribution of research outputs amongst IRRs was less even than in non-IRRs as the top 10 most studied IRRs account for 26% of papers vs 16% for non-IRRs. Out of the 10 most studied reptile species, none are island restricted (Fig. 1) and indeed, the 4 most studied reptile species total more papers than all 2438 IRRs combined.
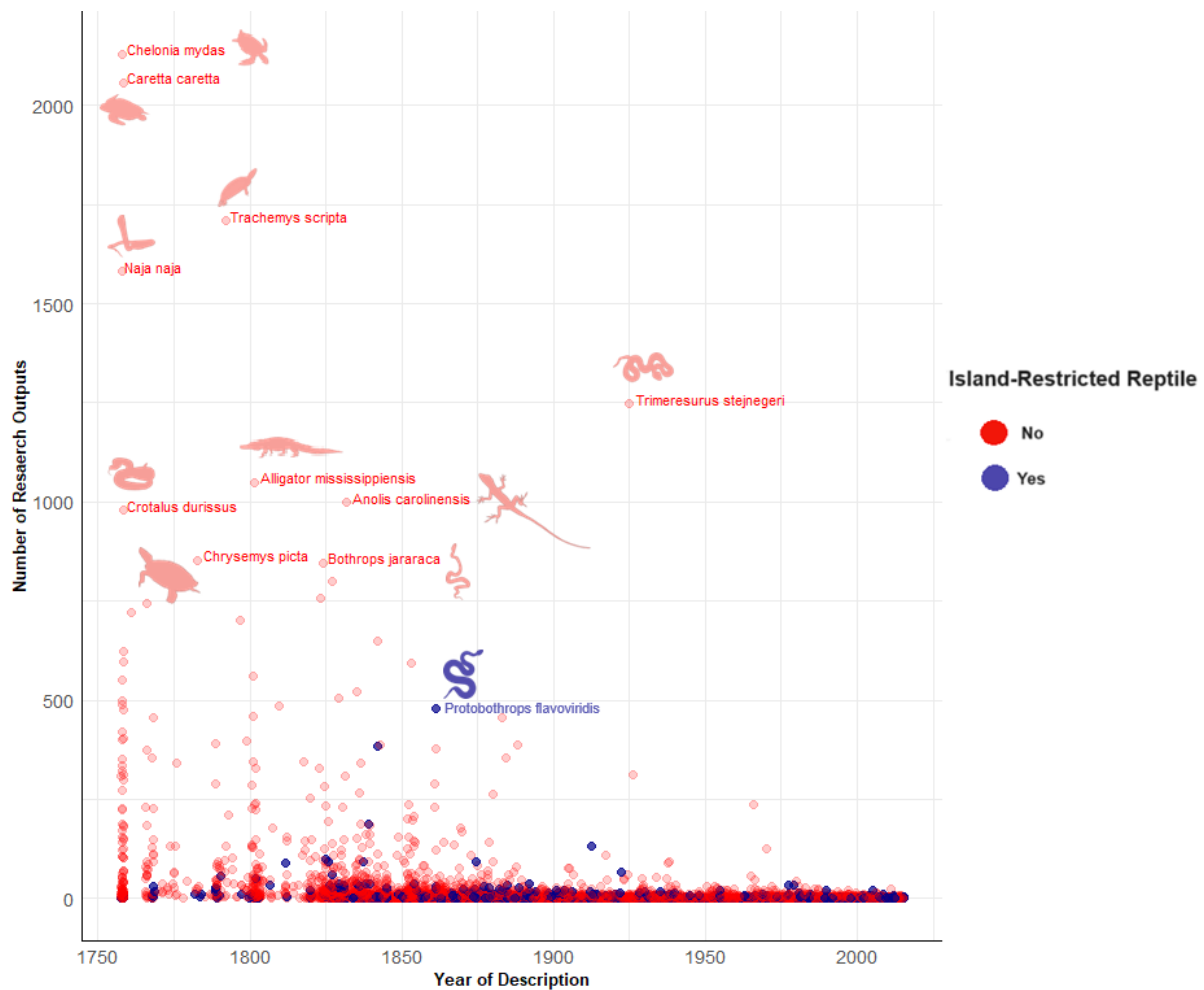
Figure 1. Total number of research outputs per reptile species, plotted against year of description. *Protobothrops flavoviridis*, the most studied Island-restricted Reptile species (n = 477 papers), is shown in blue for comparison.

3.1.2 Family-level patterns

Overall, research outputs were found to be distributed unevenly across the different reptile families. Families such as Alligatoridae or Cheloniidae have hundreds of papers per species on average (Table 2) whereas families such as Typhlopidae have a large number of species but few papers as 63.6% of Typhlopidae members have no studies at all (Table. 3). The most studied family on average was Cheloniidae (sea turtles) (n = 965.33 ± 368.25, mean ± SE) however, they are not the absolute most studied family, which was Viperidae (vipers). However, this was due to the large number of species in Viperidae, and despite having the most total studies, vipers were the tenth most studied reptile family, when considering the average number of research outputs per species (t = 16385, n = 48.19 ± 7.38,

mean ± SE, Table 2). IRRs were only present in four out of the ten most studied families and there were typically few IRRs within these four families (Table 2).

Table 2. Top 10 most studied reptile families, ranked by mean research output per species.

Family	Example Species	Mean Research Output Per Species	Number of Species	Percent of Species Found on Islands	Total Research Output	Extra Detail
Cheloniidae	Typical Sea Turtles	965.33	6	0	5792	
Dermochelyidae	Leatherback Sea Turtles	720	1	0	720	
Sphenodontidae	Tuataras*	385	1	100	385	* Of high interest for studying reptile evolution
Alligatoridae	Alligators	260.13	8	0	2081	
Chelydridae	Snapping Turtles	137.6	5	0	688	
Crocodylidae	Crocodiles*	108.69	16	18.75	1739	* 3 island species in papa new guinea, Philippines and Cuba
Emydidae	pond turtles	94.94	52	9.62	4937	
Gavialidae	Gharials	93	1	0	93	
Helodermatidae	Beaded Lizards	54.4	5	0	272	
Viperidae	Vipers	48.19	340	11.76	16385	

In contrast to the patterns observed for the reptile families with the most research outputs, IRRs are well represented in the top ten least studied families. Indeed, when ranking families by the percentage of members with no research outputs at all, we observe a high representation of IRRs within those families. Additionally, out of the ten least studied reptile families, eight have some degree of representation of IRRs and of these, five consist of over 60% IRRs. The least studied family was Cadeidae (Cuban keel-headed worms), with no identified research outputs in either of the two constituent species.

Table 3. Top 10 *least* studied reptile families, ranked by the percentage of species within that family with 0 studies.

Family	Example Species	Number of Species	Number of Species With 0 Research Outputs	Percentage of Species Found on Islands	Percentage of Species With 0 Research Outputs
Cadeidae	Cuban Keel-Headed Worms	2	2	100	100
Cyclocoridae	Philippine Burrowing Snakes	7	6	100	85.7
Gerrhopilidae	Indo-Malayan Blindsnakes	17	12	64.7	70.6
Diploglossidae	Galliwasps	49	33	49	67.3
Typhlopidae	Typical Blind Snakes	261	166	31.8	63.6
Prosymnidae	Shovel-Snout Snakes	16	10	0	62.5
Leiocephalidae	Curly-Tailed lizard	28	17	82.1	60.7
Cylindrophiidae	Asian Pipe Snakes	12	7	75	58.3
Atractaspididae	Atractaspidid Snakes	67	38	0	56.7
Leptotyphlopidae	Threadsnakes	131	71	9.9	54.2

3.1.3 Suborder patterns in research outputs among island-restricted reptiles

I also found there was a large amount of variation in the representation of different reptile suborders in the published literature relative to the proportion of threatened species in each suborder (Fig. 2). Crocodilians (Crocodylia), and wall lizards and whip tail lizards (Lacertiformes) have the highest number of research outputs in relation to the number of threatened species within the suborder. The reason for this is the few threatened species in these suborders compared to the number of research outputs. On the other hand, geckos (Gekkota), and blind skinks (Dibamidae) are the least studied as they have a low research output (Fig. S5) relative to the number of threatened species within these suborders.
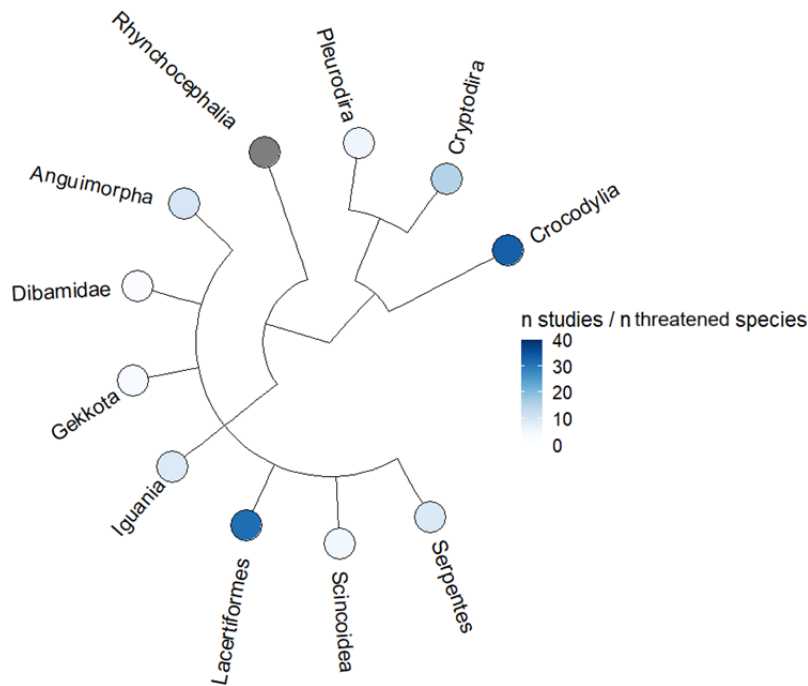
Figure 2. A phylogeny of reptile suborders only considering their island-restricted members. Branch tips are colour-coded according to the number of research outputs divided by the number of threatened species within the respective suborder. The darker the blue the higher the ratio of research output to the number of threatened species. As tuataras (Rhynchocephalia) are monophyletic and are not threatened they are featured in grey.

3.2 Covariables have similar effects on research output for island-restricted and mainland species

I found that factors that affect the number of research outputs in mainland reptile species also affect the number of research outputs of IRRs in a similar manner, albeit with slight differences in magnitude (Fig. 3). However, this was not the case for range size, which exhibited a positive effect in the number of research outputs for mainland species, but a negative effect for IRRs (Fig. 3). For both IRRs and mainland reptiles, the number of research outputs was negatively affected by year of description (meaning more recently described species had less studies), range rarity, elevation and IUCN status (with more threatened species being less studied overall). On the other hand, body mass and the number of biological institutions had positive effects on the number of research outputs each species had (Fig. 3).
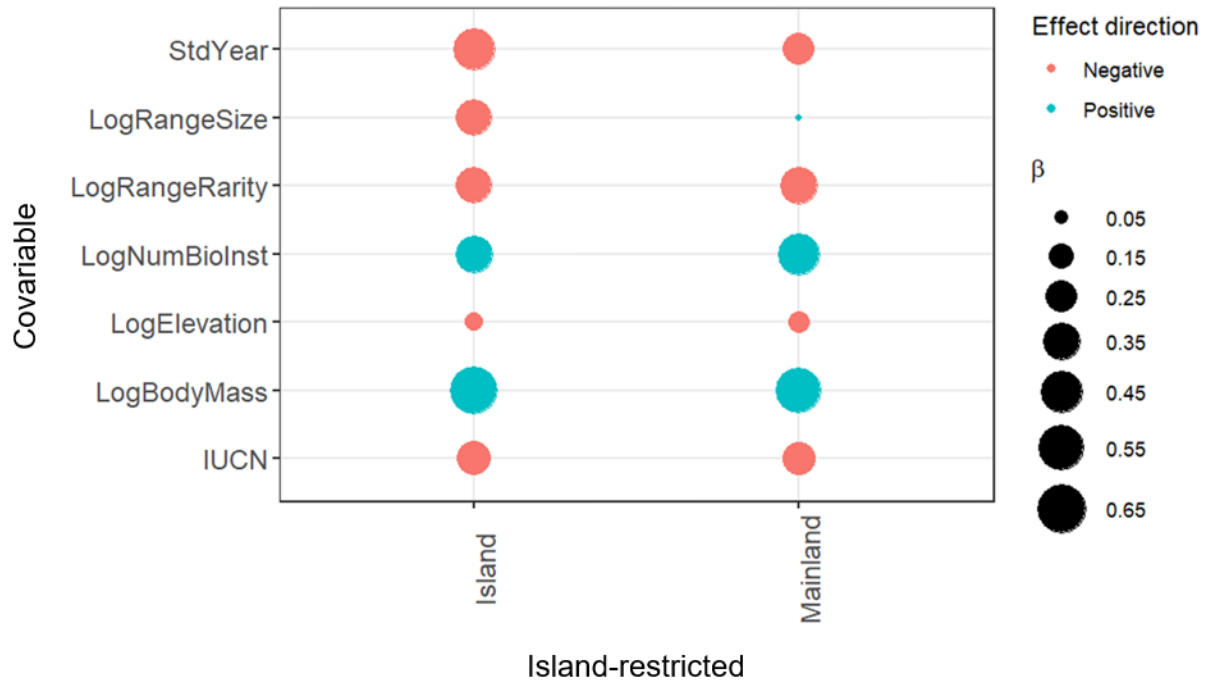
Figure 3. The effect of each covariable had on research output from the global GLMMs conducted separately on IRRs and Mainland species. The research output is modelled as a function of our covariables with the size of each dot representing the magnitude of the effect each covariable had and the colour representing the direction. IRRs had a conditional coefficient of variation R^2 value of 0.576 and a marginal of 0.441. Mainland species had a conditional coefficient of variation R^2 value of 0.730 and a marginal of 0.533.

3.3 Biogeographic realm and IUCN category may impact research output differently for island-restricted and mainland reptiles

The biogeographic realm a species resided in was found to significantly influence the number of research outputs it had (Kruskal-Wallace test; $P < 0.001$). When I investigated if IRRs and non-IRRs were affected by this factor to the same extent, the GLMMs showed that the Australasia, IndoMalay, Neartic and Neotropic realms had significantly different outputs between IRRs and non-IRRs ($P < 0.001$) (Fig. 4). The number of research outputs did not vary significantly between IRRs and non-IRRs for the other realms (Afrotropic, Oceana and Palearctic)
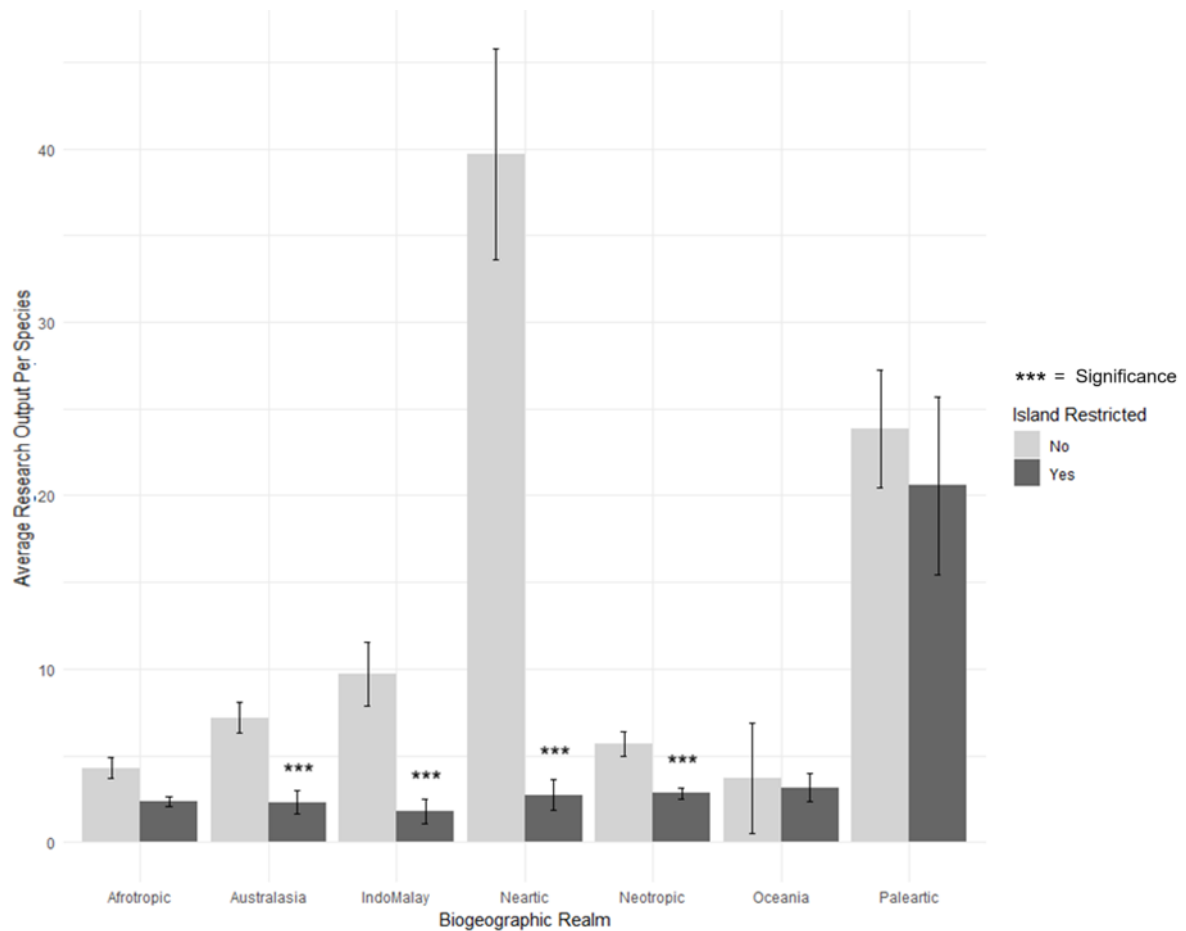
Figure 4. Mean ± SE research output per species across the different biogeographic realms. Statistically significant differences between IRRs and mainland species are indicated with *** as per the results of a post-hoc analysis.

The IUCN category of a species was found to be a significant factor affecting the number of research outputs for that species, based on a Kruskal-Wallace test ($P < 0.001$). The subsequent GLMM showed that the IUCN categories of least concern, near threatened and vulnerable had a significant difference in the number of research outputs on IRR vs non-IRRs ($P < 0.001$; Fig. 5). The other categories had less variance in the number of studies between IRRs and non-IRRs, which indicates these specific IUCN categories did not play a significant role in the disparity between IRRs and non-IRRs research output.
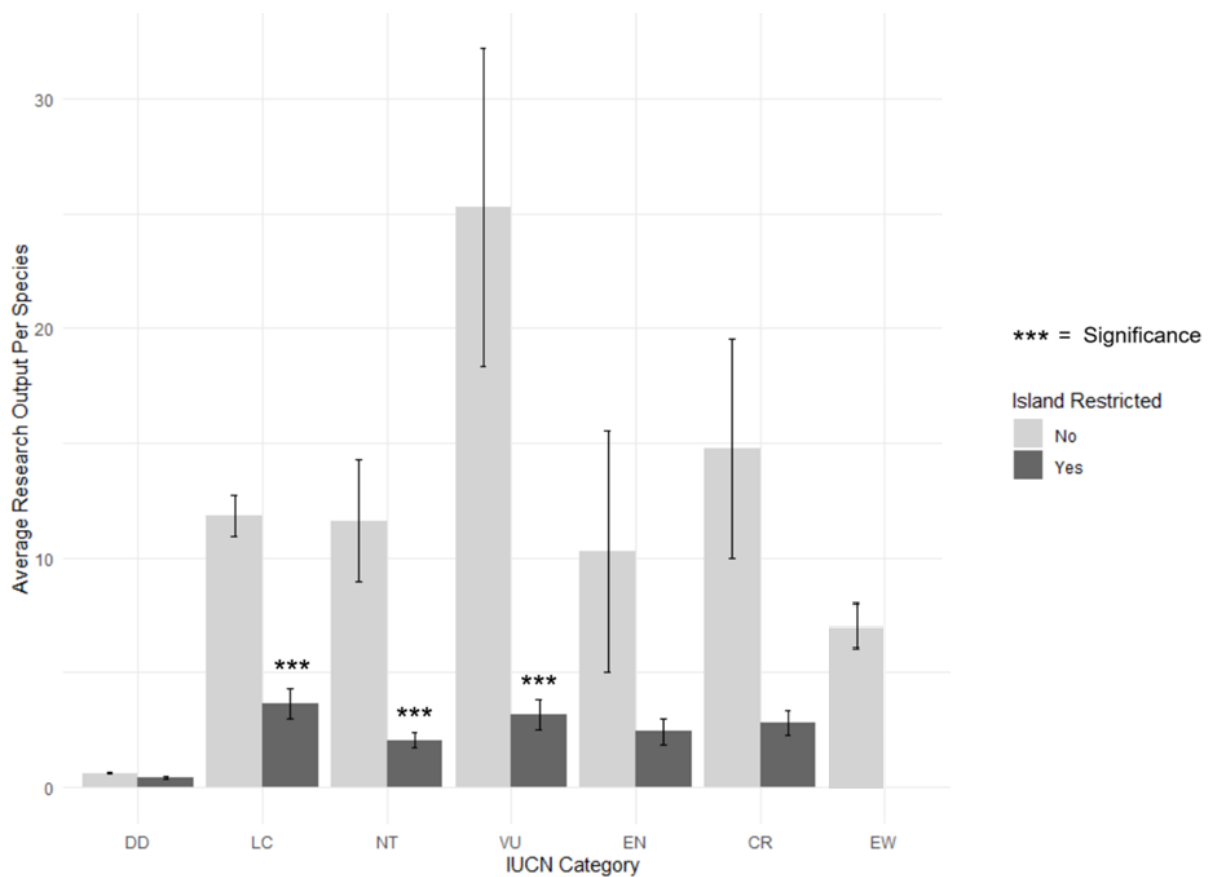
Figure 5. The mean ± SE research output for IRR and mainland species across each IUCN category (DD, Data Deficient; LC, Least Concern; NT, Near Threatened; VU, Vulnerable; EN, Endangered; CR, Critically Endangered; EW, Extinct in the Wild). The *** shows a significant result in a post-hoc analysis indicating a significant difference between the number of papers published for IRR vs mainland species within that category.

3.4 Island-restricted reptiles rank higher for future research priority

Finally, using the RPM I have ranked the top 15 reptile species most in need of research. This was a comprehensive analysis across all extant reptile's however we found that within the top 15 species most in need of research 12 of them were IRRs (Table 4). The top 11 species had a maximum RPM value of 3 (indicating that a species has no research outputs, no congeneric species and were either threatened or data deficient).

Table 4. The top 15 reptile species most in need of research ranked by Research Priority Metric (RPM)

Species	Family	Threat Status	Number of papers	Island Reptile	RPM
Anoplohydrus aemulans	Colubridae	DD	0	Yes	3
Chalcidoseps thwaitesi	Scincidae	EN	0	Yes	3
Complicitus nigrigularis	Agamidae	DD	0	Yes	3
Cyclotyphlops deharvengi	Typhlopidae	VU	0	Yes	3
Heurnia ventromaculata	Homalopsidae	DD	0	Yes	3
Karnsophis siantaris	Homalopsidae	NC	0	Yes	3
Myersophis alpestris	Cyclocoridae	DD	0	Yes	3
Sumatranus albomaculata	Homalopsidae	DD	0	Yes	3
Techmarscincus jigurru	Scincidae	VU	0	No	3
Tetralepis fruhstorferi	Colubridae	VU	0	Yes	3
Xyelodontophis uluguruensis	Colubridae	EN	0	No	3
Brygophis coulangesi	Pseudoxyrhophiidae	VU	1	Yes	2.9995
Chapinophis xanthocheilus	Colubridae	EN	1	No	2.9995
Etheridgeum pulchrum	Colubridae	DD	1	Yes	2.9995
Graciliscincus shonae	Scincidae	VU	1	Yes	2.9995

4. Discussion

In this study, I investigated how research patterns differ between island-restricted reptiles and their mainland counterparts, I found that island-restricted reptiles are underrepresented in the current scientific literature. My results show that factors – socioeconomic, geographical, physiological and conservation – identified as affecting research output in reptiles at the global scale (Guedes et al., 2023) similarly impact island-restricted reptiles, with the exception of range size. I have highlighted key island reptiles as priorities for future research, according to the Research Priority Metric. By identifying biases in the knowledge base, we can inform future research efforts allowing them to have more effective conservation outcomes (Sutherland et al., 2004).

4.1 Island-restricted reptiles have lower research output than mainland reptiles

I analysed the research output of 10,532 reptile species to determine if island-restricted reptiles (IRRs) were understudied compared to their mainland counterparts. From my analysis of the 89,280 papers published on these reptiles, I found that IRRs at the species level are studied substantially less than mainland reptiles (Fig. 1). This is similar to what we see in island-restricted birds (De Lima et al., 2011)

and bats (Conenna et al., 2017). Previous work on threatened species shows they are less studied than non-threatened species despite their greater need for study (Guy et al., 2021). Since island species are far more likely to be threatened than non-island species, (Fernández-Palacios et al., 2021; Tershy et al., 2015) the threatened status of many IRRs could be a key factor explaining the lack of research effort on IRRs compared to non-IRRs

Similarly, at the level of taxonomic family IRRs are studied less than non-IRRs. Through a simple descriptive analysis, I found IRRs are poorly represented in the most studied reptile families and well represented in the least studied families (Tables 2 & 3). Although this is what I expected based on results at the species level it is unlikely that family was the factor that predicted the research effort. Instead, it is likely that other species-level covariables are simply more prominent in those certain families making them more or less likely to be studied, as suggested by previous studies of research effort at the family level (Brooke et al., 2014). I will discuss these species-level covariables in the following sections. The implications of this are important as this is a lack of research at the family level which means it may be harder to generalise and predict what a species needs for its conservation as there are fewer closely related species that are studied to base assumptions on. The research gap that can be generated by this lack of studies at the family level can be illustrated in two families from my results. One is the most studied family (Cheloniidae, sea turtles) which has six members and 965 research outputs and the other family being one of the least studied families (Cyclocoridae, Philippine Burrowing Snakes) that has seven members but only one of these has been researched at all (Tables 2 & 3).

4.2 Covariables can cause differences in research output between Island-restricted and mainland species

I found that IRRs and mainland species were very similarly influenced by the majority of covariables I investigated, such as year of description, range rarity, number of biological institutions and elevation, with the notable exception of range size (Fig. 3). The effect direction and magnitude of these covariates did not differ between IRRs and non-IRRs (Fig. 3).

My findings that IUCN status influences research effort (species with a higher extinction risk are less well studied) is in line with the current literature, that suggests less endangered species will be generally more abundant and so are easier to find and study for both island and mainland species (Guedes et al., 2023; Schmidt et al., 2023). This theory is supported by the output we see for the range rarity covariable, which shows that the rarer a species is within its range the fewer studies were

published on it. Therefore, endangered species, which are typically less abundant and rarer within their respective range, will also be less studied. The only covariable that has substantially different effects between IRRs and non-IRRs is range size, we see that it has a negative effect on IRRs and a slight positive effect on non-IRRs. This was not expected as species spanning larger areas can hypothetically be more easily found and studied by institutions in different regions, therefore increasing their research output (Guedes et al., 2023). Our results instead indicate that IRRs on smaller islands are studied more than species on larger islands all else being equal. This may be due to smaller range sizes correlating with a higher risk of extinction and higher threat level due to smaller less stable population sizes (Matthies et al., 2004; Conenna et al., 2017) which may then result in more scientific attention for that species (Guy et al., 2021). However, this notion that smaller population sizes attract more scientific attention contradicts what is seen in many other taxonomic groups such as birds (Murray et al., 2015) and marine mammals (Jarić et al., 2015). A common trend in this research is that abundant species are more likely to be studied as they are more attractive when fundraising due to a smaller risk of failure for the research (De Lima et al., 2011). To conclude, further research is required to investigate the cause of IRRs range size negatively correlating with their research effort to help reduce the bias that currently exists.

The body mass of the species was a covariable I found to have similar effects on the research output of IRRs and non-IRRs (Fig. 3). Despite having a similar impact on both groups this covariable may still help to explain some of the research gaps observed. Based on the literature, we expect to see larger species being studied more on average due to larger body sizes which makes them easier to detect and therefore study (Gaston, 1991; Moura et al., 2018), and this is what I found. Additionally, a larger body size can also increase the charisma of and general interest in a species further contributing to a larger research output (Berti et al., 2020; Gaston, 1991; Prokop et al., 2022; Roll et al., 2016). Therefore, if larger reptiles are more often found on the mainland than on islands this could contribute to a larger research output for mainland species on average. As the evolution of larger body mass in reptiles is largely influenced by resource availability (Boback, 2003; Meiri, 2007) and as islands are often resource-restricted it would stand to reason that island species would be smaller and therefore studied less on average based on this finding. Therefore, despite an equal change in body mass having the same effect on IRRs and non-IRRs the bias in the literature towards larger species can inadvertently cause mainland species to be studied more. However, further research is needed to conclude if island species are actually smaller on average before assuming this. Investigating species that have undergone island gigantism or dwarfism may also be an interesting avenue for future study into the relationship between body mass and research output of island species.

The number of biological institutions within a reptile's range may contribute to the research gap between IRRs and non-IRRs. I found that the number of biological institutions within a species range positively correlates with the research output for both IRRs and non-IRRs (Fig. 3). As many island nations and territories lack scientific, financial and infrastructure resources (Reaser et al., 2007) we may see a decrease in funding (Bruner et al., 2004) for biological institutions on islands compared to mainlands. This will therefore have a negative impact on the research output of island species, helping to contribute to the research gap we see. This is why it is fundamental that well-funded mainland scientific institutions and governments aid in the development of these island nations and territories. By doing this it can enable the people on islands which contain such unique reptile fauna to create the backbone of scientific literature to support future conservation efforts.

Another factor that may contribute to the large research gap between island-restricted and mainland species is what biogeographic realm that species is found in. The average number of studies per species differs between island-restricted and mainland species in each realm (Fig. 4). The region with the largest difference in studies is the Nearctic. The Nearctic has an unusually low number of studies for IRRs considering the region consists primarily of Noth America which has a high capacity for research due to its high GDP. Compared to the Palearctic, which has a similar number of IRRs and mainland species (Fig. S4) as well as containing Europe, another high-income region the Nearctic has a far lower number of studies for IRRs compared to non-IRRs (Fig. 4). This disparity may require further research to understand as on the surface both the Palearctic and the Nearctic share many similarities and yet their average research outputs differ greatly. In contrast, the Afrotropic realm has one of the smallest differences in research output between IRRs and non-IRRs (Fig. 4). The Afrotropic realm is generally understudied (Farooq et al., 2021), meaning that the difference in research between the IRRs and non-IRRs is not as great. This is concerning as it highlights the lack of research in sub-Saharan Africa in general. The Afrotropics contain Madagascar one of the most reptile-diverse islands globally (The Reptile Database, 2024) with 90% of them being endemic (Convention on Biological Diversity, 2024) and so increasing research attention for Africa as a whole could be a solution that leads to Madagascar and all its endemic reptiles being studied more.

4.3 Future reptile research should prioritise island-restricted species

Based on the research priority metric I used to rank species most in need of study I found that IRRs rank highly compared to mainland species and so are generally more understudied and in need of conservation. IRRs are disproportionately represented in the species with the highest RPM scores comprising twelve of the top fifteen species most in need of study (Table. 4). This was expected as the

island species are more threatened than those on the mainland (Fernández-Palacios et al., 2021) and have been shown in other taxonomic groups to have less research output (Conenna et al., 2017; De Lima et al., 2011) which are both important factors when calculating the RPM. Arguing for further research and conservation of these high RPM species is important as they are the ones that would benefit the most from being studied. This is because the least is known about them, they are the ones most likely to go extinct without any intervention, and their extinction may confer a high loss of phylogenetic diversity, as indicated by their taxonomic distinctiveness. Furthermore, seven out of fifteen of these species are data deficient or not categorised by the IUCN, this can be detrimental to their conservation. This is because some species will not be included in conservation legislation unless they are categorised as threatened (Cazalis et al., 2023) which 21% of data deficient squamates are (Wotherspoon et al., 2024). Reptiles represent a vast amount of genetic diversity (Cox et al., 2022) comprising a substantial and important section of the tree of life, this diversity may be even higher on oceanic islands (Hébert et al., 2021) which makes them intrinsically valuable for conservation (Gumbs et al., 2020). Therefore, species ranking highly on the RPM which similarly have high levels of phylogenetic uniqueness, often being monophyletic, are also important for conservation (Cardillo, 2023) and thus should be prioritised for future research.

IRRS have a mean of 2.7 papers per species on average, this is far lower than other taxonomic groups. If we want to have accurate and effective conservation outcomes for these species we require an increased amount of research effort overall so that information relevant to their conservation is available to policy makers. Birds for example possess a mean of 96 papers per species (Murray et al., 2015) allowing for a far richer knowledge of each species to inform their conservation. While this may be a large task even increasing the mean number of studies for IRRs to the level of non-IRRs (10.4 papers per species) would bring a valuable amount of knowledge needed in order to conserve these species.

A limitation of this study may also seen in how we found the research output for each species. Relying on the database used in Guedes et al., 2023 was time effective however as it relied exclusively on the Scopus database for information on research output some data may be unintentionally omitted such as sources that are not present in Scopus or others such as grey literature. For a more complete knowledge gap analysis collating multiple databases such as Scopus, Web of Science and Google Scholar may result in a more holistic overview and accurate research output.

4.4 Conclusion

With reptiles being understudied as a class of animal compared to birds or mammals (Pilliod et al., 2023) and island-restricted reptiles being an even more neglected subgroup as concluded by our findings (Fig. 1, Table. 2 & 3) it is no wonder that they are going extinct on islands at a such a high rate (89% of known reptile extinctions (Fernández-Palacios et al., 2021)). To help reduce the loss of the world's island-restricted reptiles at a global level we must increase the research effort on island-restricted species with a particular focus on those that are poorly studied and those that are threatened. To close the knowledge gap between island-restricted and mainland reptiles we must extend the capacity and knowledge developed from studying mainland reptiles to help improve the studies of those restricted to islands, broadening the scope of herpetological research to be more inclusive of island-restricted species. Additionally, more must be learnt about the threatened and data deficient species of IRRs, especially those at the extremes which rank highest in the research priority metric, so effective conservation action can be carried out when needed. By conserving reptile biodiversity on islands we can help to conserve the systems and processes they play a critical role in. By addressing the causes for this imbalance in research effort between island-restricted and mainland reptiles we can help to eliminate the root causes for this research gap and so prevent it from growing. I recommend concurrent prioritisation of investment and increased capacity for future island-restricted reptile research, in order to help reduce this knowledge gap. If this cannot be accomplished, we will lack the evidence base for targeted conservation interventions when we need them, leading to the loss of species before we can understand them.

Acknowledgements

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Management Report

This project was originally meant to be an investigation into the effects of the environment and biological interactions on the abundance of an island-restricted lizard, this was changed significantly due to the data collection not being able to be carried out. The fieldwork portion of this project which took place in September 2023 could not be completed as planned due to unforeseen weather conditions in the mountains causing a lack of lizard activity. As we could not monitor or collect abundance data for the lizards we were forced to change the direction of the project substantially.

Having used all of my resaerch grant on the previous fieldwork I had no more funds remaining for another experimental project involving lizards. Due to this, I changed the course of my project, instead choosing a desk-based knowledge gap analysis at the suggestion of supervisor Ricardo Rocha. For the first few weeks of Michaelmas term, I familiarised myself with the idea of a knowledge gap analysis and looked into the previous work of Ricardo as he had been involved in a similar project on bats. I then spent the remainder of Michaelmas term learning data analysis techniques in R some of which built on what I had learnt in Andy Hectors coding classes and some that I had to teach myself. Similarly, I also learnt the basics of ArcGIS and how to manage large datasets in Excel which I was not previously familiar with.

I spent Hillary term carrying out data analysis as I was now much more comfortable in R using general linear mixed models, cleaning and wrangling the data, conducting multiple comparisons and data dredging. I continued my literature review during this time to deepen my understanding of past knowledge gap analyses and what types of questions I should be asking. By the start of April, I had completed this process and had most of the statistical analysis completed and I also had a good idea of what I wanted this project to look like. I then started writing my dissertation and finalising the graphs

and tables I would use as my figures. Unfortunately, Ricardo was on the 2nd year Borneo field course in the last two weeks before the deadline but I was able to submit a semi-final draft before then to get as much feedback as possible. With the help of my co-supervisor Phoebe Griffith, I was able to submit a final draft by the deadline.

Appendix

S1. Outputs of the GLMM on the IUCN statuses

Summary table

```
Generalized linear mixed model fit by maximum likelihood (Laplace
Approximation) ['glmerMod']
 Family: Negative Binomial(1)  ( log )
Formula: Npapers1stApproach ~ ThreatStatus_Plus + (1 | Family)
   Data: AllReptiles
```

AIC	BIC	logLik	deviance	df.resid
51459.2	51597.2	-25710.6	51421.2	10512

```
Scaled residuals:
```

Min	1Q	Median	3Q	Max
-0.99	-0.81	-0.61	-0.11	340.56

```
Random effects:
```

Groups	Name	Variance	Std.Dev.
Family	(Intercept)	2.739	1.655

```
Number of obs: 10531, groups:  Family, 92
```

Fixed effects:

	Estimate	Std. Error	z value	Pr(>|z|)	
(Intercept)	0.75088	0.20219	3.714	0.000204	***
ThreatStatus_PlusCR__Mainland	0.20037	0.13474	1.487	0.136992	
ThreatStatus_PlusDD__Island	-1.03388	0.15554	-6.647	2.99E-11	***
ThreatStatus_PlusDD__Mainland	-0.72559	0.11606	-6.252	4.05E-10	***
ThreatStatus_PlusEN__Island	0.32331	0.1209	2.674	0.007488	**
ThreatStatus_PlusEN__Mainland	0.51465	0.11508	4.472	7.75E-06	***
ThreatStatus_PlusEW__Mainland	1.90491	0.76247	2.498	0.012477	*
ThreatStatus_PlusEX__Island	1.93431	1.04703	1.847	0.064684	.
ThreatStatus_PlusEX__Mainland	0.72202	0.28825	2.505	0.012252	*
ThreatStatus_PlusLC__Island	0.72361	0.10367	6.98	2.95E-12	***
ThreatStatus_PlusLC__Mainland	1.62059	0.09792	16.55	< 2e-16	***
ThreatStatus_PlusNC__Island	-1.04900	0.15891	-6.601	4.07E-11	***
ThreatStatus_PlusNC__Mainland	0.27012	0.10498	2.573	0.010078	*

ThreatStatus_PlusNT__Island 0.37441	0.13206	2.835	0.00458	**
ThreatStatus_PlusNT__Mainland 0.91972	0.11546	7.965	1.65E-15	***
ThreatStatus_PlusVU__Island 0.27114	0.12865	2.108	0.035073	*
ThreatStatus_PlusVU__Mainland 1.12868	0.11367	9.93	< 2e-16	***

```
---
Signif. codes:  0 '***'
0.001 '**' 0.0            1 '*        ' 0.05    '.' 0.1  ' ' 1
```
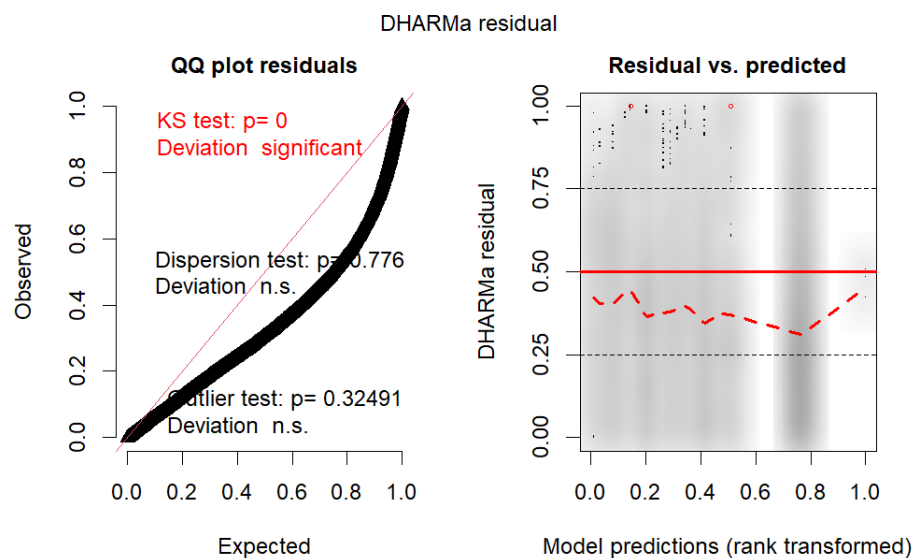
Residuals

DHARMa residual

Multiple comparisons

```
Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts


Fit: glmer(formula = Npapers1stApproach ~ ThreatStatus_Plus + (1 |
    Family), data = AllReptiles, family = negative.binomial(theta = 1))

Linear Hypotheses:
```

	Estimate	Std. Error	z value	Pr(>|z|)	
CR__Mainland - CR__Island == 0	0.200372	0.134741	1.487	0.9793	
DD__Island - CR__Island == 0	-1.033882	0.155536	-6.647	<0.01	***
DD__Mainland - CR__Island == 0	-0.725587	0.116057	-6.252	<0.01	***
EN__Island - CR__Island == 0	0.323315	0.120896	2.674	0.2936	
EN__Mainland - CR__Island == 0	0.514648	0.115080	4.472	<0.01	***
EW__Mainland - CR__Island == 0	1.904909	0.762467	2.498	0.4121	
EX__Island - CR__Island == 0	1.934315	1.047028	1.847	0.8730	
EX__Mainland - CR__Island == 0	0.722020	0.288253	2.505	0.4077	
LC__Island - CR__Island == 0	0.723607	0.103669	6.980	<0.01	***
LC__Mainland - CR__Island == 0	1.620585	0.097919	16.550	<0.01	***

```
NC__Island - CR__Island == 0       -1.049003  0.158905  -6.601   <0.01 ***
NC__Mainland - CR__Island == 0      0.270119  0.104976   2.573   0.3591
NT__Island - CR__Island == 0        0.374415  0.132061   2.835   0.2054
NT__Mainland - CR__Island == 0      0.919720  0.115463   7.965   <0.01 ***
VU__Island - CR__Island == 0        0.271141  0.128654   2.108   0.7131
VU__Mainland - CR__Island == 0      1.128682  0.113666   9.930   <0.01 ***
DD__Island - CR__Mainland == 0     -1.234255  0.155840  -7.920   <0.01 ***
DD__Mainland - CR__Mainland == 0   -0.925959  0.115915  -7.988   <0.01 ***
EN__Island - CR__Mainland == 0      0.122942  0.121886   1.009   0.9997
EN__Mainland - CR__Mainland == 0    0.314276  0.111956   2.807   0.2170
EW__Mainland - CR__Mainland == 0    1.704537  0.762761   2.235   0.6156
EX__Island - CR__Mainland == 0      1.733942  1.047077   1.656   0.9451
EX__Mainland - CR__Mainland == 0    0.521648  0.287976   1.811   0.8891
LC__Island - CR__Mainland == 0      0.523235  0.104540   5.005   <0.01 ***
LC__Mainland - CR__Mainland == 0    1.420213  0.097654  14.543   <0.01 ***
NC__Island - CR__Mainland == 0     -1.249375  0.159043  -7.856   <0.01 ***
NC__Mainland - CR__Mainland == 0    0.069747  0.103821   0.672   1.0000
NT__Island - CR__Mainland == 0      0.174042  0.132397   1.315   0.9941
NT__Mainland - CR__Mainland == 0    0.719348  0.113912   6.315   <0.01 ***
VU__Island - CR__Mainland == 0      0.070768  0.129981   0.544   1.0000
VU__Mainland - CR__Mainland == 0    0.928310  0.110639   8.390   <0.01 ***
DD__Mainland - DD__Island == 0      0.308295  0.137697   2.239   0.6134
EN__Island - DD__Island == 0        1.357197  0.142736   9.508   <0.01 ***
EN__Mainland - DD__Island == 0      1.548531  0.137825  11.236   <0.01 ***
EW__Mainland - DD__Island == 0      2.938791  0.766415   3.834   <0.01 **
EX__Island - DD__Island == 0        2.968197  1.049587   2.828   0.2075
EX__Mainland - DD__Island == 0      1.755903  0.298367   5.885   <0.01 ***
LC__Island - DD__Island == 0        1.757489  0.128353  13.693   <0.01 ***
LC__Mainland - DD__Island == 0      2.654468  0.123336  21.522   <0.01 ***
NC__Island - DD__Island == 0       -0.015121  0.175153  -0.086   1.0000
NC__Mainland - DD__Island == 0      1.304001  0.128943  10.113   <0.01 ***
NT__Island - DD__Island == 0        1.408297  0.152275   9.248   <0.01 ***
NT__Mainland - DD__Island == 0      1.953602  0.137751  14.182   <0.01 ***
VU__Island - DD__Island == 0        1.305023  0.150358   8.679   <0.01 ***
VU__Mainland - DD__Island == 0      2.162564  0.136410  15.853   <0.01 ***
EN__Island - DD__Mainland == 0      1.048901  0.098815  10.615   <0.01 ***
EN__Mainland - DD__Mainland == 0    1.240235  0.090015  13.778   <0.01 ***
EW__Mainland - DD__Mainland == 0    2.630496  0.759488   3.464   0.0327 *
EX__Island - DD__Mainland == 0      2.659901  1.044552   2.546   0.3777
EX__Mainland - DD__Mainland == 0    1.447607  0.279917   5.172   <0.01 ***
LC__Island - DD__Mainland == 0      1.449194  0.075961  19.078   <0.01 ***
LC__Mainland - DD__Mainland == 0    2.346172  0.066035  35.529   <0.01 ***
NC__Island - DD__Mainland == 0     -0.323416  0.141876  -2.280   0.5803
NC__Mainland - DD__Mainland == 0    0.995706  0.076521  13.012   <0.01 ***
NT__Island - DD__Mainland == 0      1.100001  0.111754   9.843   <0.01 ***
NT__Mainland - DD__Mainland == 0    1.645307  0.090619  18.156   <0.01 ***
VU__Island - DD__Mainland == 0      0.996727  0.109307   9.119   <0.01 ***
VU__Mainland - DD__Mainland == 0    1.854269  0.088165  21.032   <0.01 ***
EN__Mainland - EN__Island == 0      0.191334  0.097693   1.959   0.8124
EW__Mainland - EN__Island == 0      1.581594  0.760273   2.080   0.7321
EX__Island - EN__Island == 0        1.611000  1.045246   1.541   0.9710
EX__Mainland - EN__Island == 0      0.398706  0.282049   1.414   0.9874
LC__Island - EN__Island == 0        0.400292  0.083636   4.786   <0.01 ***
LC__Mainland - EN__Island == 0      1.297271  0.076656  16.923   <0.01 ***
NC__Island - EN__Island == 0       -1.372317  0.146314  -9.379   <0.01 ***
NC__Mainland - EN__Island == 0     -0.053196  0.085774  -0.620   1.0000
NT__Island - EN__Island == 0        0.051100  0.116543   0.438   1.0000
NT__Mainland - EN__Island == 0      0.596406  0.097949   6.089   <0.01 ***
VU__Island - EN__Island == 0       -0.052174  0.113450  -0.460   1.0000
VU__Mainland - EN__Island == 0      0.805367  0.096576   8.339   <0.01 ***
EW__Mainland - EN__Mainland == 0    1.390261  0.759364   1.831   0.8805
EX__Island - EN__Mainland == 0      1.419666  1.044587   1.359   0.9915
EX__Mainland - EN__Mainland == 0    0.207372  0.279494   0.742   1.0000
LC__Island - EN__Mainland == 0      0.208959  0.074918   2.789   0.2290
LC__Mainland - EN__Mainland == 0    1.105937  0.064892  17.043   <0.01 ***
NC__Island - EN__Mainland == 0     -1.563651  0.141418 -11.057   <0.01 ***
NC__Mainland - EN__Mainland == 0   -0.244529  0.075374  -3.244   0.0677 .
NT__Island - EN__Mainland == 0     -0.140234  0.110872  -1.265   0.9961
NT__Mainland - EN__Mainland == 0    0.405072  0.088832   4.560   <0.01 ***
```

```
VU__Island - EN__Mainland == 0    -0.243508   0.108290  -2.249    0.6050
VU__Mainland - EN__Mainland == 0   0.614034   0.086213   7.122    <0.01 ***
EX__Island - EW__Mainland == 0     0.029406   1.288048   0.023    1.0000
EX__Mainland - EW__Mainland == 0  -1.182889   0.803868  -1.471    0.9811
LC__Island - EW__Mainland == 0    -1.181302   0.757621  -1.559    0.9673
LC__Mainland - EW__Mainland == 0  -0.284324   0.756912  -0.376    1.0000
NC__Island - EW__Mainland == 0    -2.953912   0.767071  -3.851    <0.01 **
NC__Mainland - EW__Mainland == 0  -1.634790   0.757748  -2.157    0.6745
NT__Island - EW__Mainland == 0    -1.530494   0.762042  -2.008    0.7807
NT__Mainland - EW__Mainland == 0  -0.985189   0.759515  -1.297    0.9949
VU__Island - EW__Mainland == 0    -1.633768   0.761623  -2.145    0.6834
VU__Mainland - EW__Mainland == 0  -0.776227   0.759187  -1.022    0.9997
EX__Mainland - EX__Island == 0    -1.212294   1.077382  -1.125    0.9990
LC__Island - EX__Island == 0      -1.210708   1.043327  -1.160    0.9985
LC__Mainland - EX__Island == 0    -0.313729   1.042783  -0.301    1.0000
NC__Island - EX__Island == 0      -2.983318   1.050065  -2.841    0.2028
NC__Mainland - EX__Island == 0    -1.664196   1.043070  -1.595    0.9599
NT__Island - EX__Island == 0      -1.559900   1.046543  -1.491    0.9788
NT__Mainland - EX__Island == 0    -1.014595   1.044631  -0.971    0.9998
VU__Island - EX__Island == 0      -1.663174   1.046163  -1.590    0.9616
VU__Mainland - EX__Island == 0    -0.805633   1.044421  -0.771    1.0000
LC__Island - EX__Mainland == 0     0.001587   0.274542   0.006    1.0000
LC__Mainland - EX__Mainland == 0   0.898565   0.272855   3.293    0.0584 .
NC__Island - EX__Mainland == 0    -1.771023   0.299705  -5.909    <0.01 ***
NC__Mainland - EX__Mainland == 0  -0.451901   0.274239  -1.648    0.9473
NT__Island - EX__Mainland == 0    -0.347606   0.286739  -1.212    0.9976
NT__Mainland - EX__Mainland == 0   0.197700   0.279505   0.707    1.0000
VU__Island - EX__Mainland == 0    -0.450880   0.284987  -1.582    0.9630
VU__Mainland - EX__Mainland == 0   0.406661   0.278810   1.459    0.9827
LC__Mainland - LC__Island == 0     0.896978   0.043483  20.628    <0.01 ***
NC__Island - LC__Island == 0      -1.772610   0.132211 -13.407    <0.01 ***
NC__Mainland - LC__Island == 0    -0.453488   0.057851  -7.839    <0.01 ***
NT__Island - LC__Island == 0      -0.349192   0.098056  -3.561    0.0248 *
NT__Mainland - LC__Island == 0     0.196113   0.075523   2.597    0.3425
VU__Island - LC__Island == 0      -0.452466   0.095547  -4.736    <0.01 ***
VU__Mainland - LC__Island == 0     0.405075   0.073173   5.536    <0.01 ***
NC__Island - LC__Mainland == 0    -2.669588   0.127721 -20.902    <0.01 ***
NC__Mainland - LC__Mainland == 0  -1.350466   0.045087 -29.952    <0.01 ***
NT__Island - LC__Mainland == 0    -1.246171   0.092772 -13.433    <0.01 ***
NT__Mainland - LC__Mainland == 0  -0.700865   0.065578 -10.688    <0.01 ***
VU__Island - LC__Mainland == 0    -1.349445   0.089653 -15.052    <0.01 ***
VU__Mainland - LC__Mainland == 0  -0.491903   0.062341  -7.891    <0.01 ***
NC__Mainland - NC__Island == 0     1.319122   0.132635   9.946    <0.01 ***
NT__Island - NC__Island == 0       1.423418   0.155657   9.145    <0.01 ***
NT__Mainland - NC__Island == 0     1.968723   0.141464  13.917    <0.01 ***
VU__Island - NC__Island == 0       1.320144   0.153788   8.584    <0.01 ***
VU__Mainland - NC__Island == 0     2.177685   0.140361  15.515    <0.01 ***
NT__Island - NC__Mainland == 0     0.104296   0.100144   1.041    0.9996
NT__Mainland - NC__Mainland == 0   0.649601   0.076014   8.546    <0.01 ***
VU__Island - NC__Mainland == 0     0.001022   0.097057   0.011    1.0000
VU__Mainland - NC__Mainland == 0   0.858563   0.073477  11.685    <0.01 ***
NT__Mainland - NT__Island == 0     0.545305   0.111405   4.895    <0.01 ***
VU__Island - NT__Island == 0      -0.103274   0.125172  -0.825    1.0000
VU__Mainland - NT__Island == 0     0.754267   0.109746   6.873    <0.01 ***
VU__Island - NT__Mainland == 0    -0.648579   0.108638  -5.970    <0.01 ***
VU__Mainland - NT__Mainland == 0   0.208962   0.086359   2.420    0.4687
VU__Mainland - VU__Island == 0     0.857541   0.106971   8.017    <0.01 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)
```

S.2 Output of the GLMM on the biogeographic realms

Summary table

```
Generalized linear mixed model fit by maximum likelihood (Laplace
Approximation) ['glmerMod']
 Family: Negative Binomial(1)  ( log )
Formula: Npapers1stApproach ~ RealmPlus + (1 | Family)
   Data: AllReptiles

     AIC      BIC   logLik deviance df.resid
 50747.5   50870.9  -25356.7   50713.5     10514

Scaled residuals:
   Min     1Q Median     3Q    Max
-0.998 -0.822 -0.632 -0.057 74.154

Random effects:
 Groups Name          Variance Std.Dev.
 Family (Intercept) 2.372    1.54
Number of obs: 10531, groups:  Family, 92

Fixed effects:
                             Estimate Std. Error z value Pr(>|z|)
(Intercept)                  1.329482   0.178817   7.435 1.05e-13 ***
RealmPlusAfrotropic__Mainland -0.005116   0.072572  -0.070   0.9438
RealmPlusAustralasi__Island  -0.435097   0.089419  -4.866 1.14e-06 ***
RealmPlusAustralasi__Mainland 0.841125   0.078142  10.764  < 2e-16 ***
RealmPlusIndoMalay__Island   -0.923475   0.088120 -10.480  < 2e-16 ***
RealmPlusIndoMalay__Mainland  0.558666   0.075255   7.424 1.14e-13 ***
RealmPlusNA                  -0.587506   0.085350  -6.883 5.84e-12 ***
RealmPlusNeartic__Island     -0.143216   0.268547  -0.533   0.5938
RealmPlusNeartic__Mainland    2.155556   0.090728  23.758  < 2e-16 ***
RealmPlusNeotropic__Island   -0.225872   0.096244  -2.347   0.0189 *
RealmPlusNeotropic__Mainland  0.198824   0.077560   2.563   0.0104 *
RealmPlusOceania__Island      0.357218   0.191273   1.868   0.0618 .
RealmPlusOceania__Mainland    0.704021   0.664937   1.059   0.2897
RealmPlusPaleartic__Island    1.983589   0.176345  11.248  < 2e-16 ***
RealmPlusPaleartic__Mainland  1.813889   0.081484  22.261  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
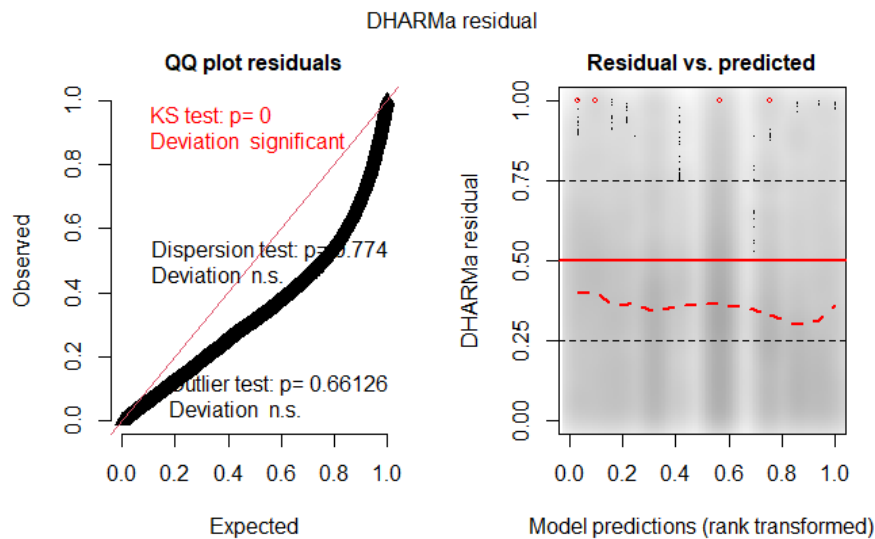
Residuals

DHARMa residual

QQ plot residuals

KS test: p= 0
Deviation significant

Dispersion test: p=0.774
Deviation n.s.

Outlier test: p= 0.66126
Deviation n.s.

Observed / Expected

Residual vs. predicted

DHARMa residual / Model predictions (rank transformed)

Multiple Comparisons

Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts

Fit: glmer(formula = Npapers1stApproach ~ RealmPlus + (1 | Family),
    data = AllReptiles, family = negative.binomial(theta = 1))

Linear Hypotheses:

	Estimate	Std. Error	z value	Pr(>|z|)	
Afrotropic__Mainland - Afrotropic__Island == 0	-0.005116	0.072572	-0.070	1.0000	
Australasi__Island - Afrotropic__Island == 0	-0.435097	0.089419	-4.866	<0.01	***
Australasi__Mainland - Afrotropic__Island == 0	0.841125	0.078142	10.764	<0.01	***
IndoMalay__Island - Afrotropic__Island == 0	-0.923475	0.088120	-10.480	<0.01	***
IndoMalay__Mainland - Afrotropic__Island == 0	0.558666	0.075255	7.424	<0.01	***
NA - Afrotropic__Island == 0	-0.587506	0.085350	-6.883	<0.01	***
Neartic__Island - Afrotropic__Island == 0	-0.143216	0.268547	-0.533	1.0000	
Neartic__Mainland - Afrotropic__Island == 0	2.155556	0.090728	23.758	<0.01	***
Neotropic__Island - Afrotropic__Island == 0	-0.225872	0.096244	-2.347	0.4784	
Neotropic__Mainland - Afrotropic__Island == 0	0.198824	0.077560	2.563	0.3245	
Oceania__Island - Afrotropic__Island == 0	0.357218	0.191273	1.868	0.8229	
Oceania__Mainland - Afrotropic__Island == 0	0.704021	0.664937	1.059	0.9988	
Paleartic__Island - Afrotropic__Island == 0	1.983589	0.176345	11.248	<0.01	***
Paleartic__Mainland - Afrotropic__Island == 0	1.813889	0.081484	22.261	<0.01	***
Australasi__Island - Afrotropic__Mainland == 0	-0.429981	0.069720	-6.167	<0.01	***
Australasi__Mainland - Afrotropic__Mainland == 0	0.846241	0.054199	15.614	<0.01	***
IndoMalay__Island - Afrotropic__Mainland == 0	-0.918359	0.067895	-13.526	<0.01	***
IndoMalay__Mainland - Afrotropic__Mainland == 0	0.563782	0.049758	11.330	<0.01	***
NA - Afrotropic__Mainland == 0	-0.582390	0.062633	-9.298	<0.01	***
Neartic__Island - Afrotropic__Mainland == 0	-0.138100	0.262308	-0.526	1.0000	
Neartic__Mainland - Afrotropic__Mainland == 0	2.160672	0.069949	30.889	<0.01	***
Neotropic__Island - Afrotropic__Mainland == 0	-0.220756	0.077321	-2.855	0.1683	
Neotropic__Mainland - Afrotropic__Mainland == 0	0.203940	0.051712	3.944	<0.01	**
Oceania__Island - Afrotropic__Mainland == 0	0.362334	0.183302	1.977	0.7535	
Oceania__Mainland - Afrotropic__Mainland == 0	0.709137	0.663006	1.070	0.9986	
Paleartic__Island - Afrotropic__Mainland == 0	1.988705	0.166519	11.943	<0.01	***
Paleartic__Mainland - Afrotropic__Mainland == 0	1.819005	0.058271	31.216	<0.01	***
Australasi__Mainland - Australasi__Island == 0	1.276222	0.067354	18.948	<0.01	***
IndoMalay__Island - Australasi__Island == 0	-0.488379	0.082520	-5.918	<0.01	***
IndoMalay__Mainland - Australasi__Island == 0	0.993763	0.069414	14.317	<0.01	***
NA - Australasi__Island == 0	-0.152409	0.079762	-1.911	0.7972	
Neartic__Island - Australasi__Island == 0	0.291881	0.266690	1.094	0.9983	
Neartic__Mainland - Australasi__Island == 0	2.590653	0.085582	30.271	<0.01	***
Neotropic__Island - Australasi__Island == 0	0.209225	0.091824	2.279	0.5306	
Neotropic__Mainland - Australasi__Island == 0	0.633921	0.071882	8.819	<0.01	***
Oceania__Island - Australasi__Island == 0	0.792314	0.187483	4.226	<0.01	**
Oceania__Mainland - Australasi__Island == 0	1.139118	0.664775	1.714	0.8989	

```
Paleartic__Island - Australasi__Island == 0       2.418686  0.174001  13.900  <0.01 ***
Paleartic__Mainland - Australasi__Island == 0     2.248986  0.077614  28.977  <0.01 ***
IndoMalay__Island - Australasi__Mainland == 0    -1.764600  0.069927 -25.235  <0.01 ***
IndoMalay__Mainland - Australasi__Mainland == 0  -0.282459  0.053476  -5.282  <0.01 ***
NA - Australasi__Mainland == 0                   -1.428631  0.066305 -21.546  <0.01 ***
Neartic__Island - Australasi__Mainland == 0      -0.984341  0.263057  -3.742  0.0105 *
Neartic__Mainland - Australasi__Mainland == 0     1.314431  0.073294  17.934  <0.01 ***
Neotropic__Island - Australasi__Mainland == 0    -1.066997  0.080476 -13.259  <0.01 ***
Neotropic__Mainland - Australasi__Mainland == 0  -0.642301  0.056567 -11.355  <0.01 ***
Oceania__Island - Australasi__Mainland == 0      -0.483907  0.182749  -2.648  0.2721
Oceania__Mainland - Australasi__Mainland == 0    -0.137104  0.663327  -0.207  1.0000
Paleartic__Island - Australasi__Mainland == 0     1.142464  0.168372   6.785  <0.01 ***
Paleartic__Mainland - Australasi__Mainland == 0   0.972764  0.063613  15.292  <0.01 ***
IndoMalay__Mainland - IndoMalay__Island == 0      1.482142  0.065972  22.466  <0.01 ***
NA - IndoMalay__Island == 0                       0.335970  0.077143   4.355  <0.01 **
Neartic__Island - IndoMalay__Island == 0          0.780260  0.265928   2.934  0.1373
Neartic__Mainland - IndoMalay__Island == 0        3.079032  0.082399  37.367  <0.01 ***
Neotropic__Island - IndoMalay__Island == 0        0.697604  0.089381   7.805  <0.01 ***
Neotropic__Mainland - IndoMalay__Island == 0      1.122299  0.067872  16.536  <0.01 ***
Oceania__Island - IndoMalay__Island == 0          1.280693  0.188569   6.792  <0.01 ***
Oceania__Mainland - IndoMalay__Island == 0        1.627497  0.664499   2.449  0.3991
Paleartic__Island - IndoMalay__Island == 0        2.907064  0.172560  16.847  <0.01 ***
Paleartic__Mainland - IndoMalay__Island == 0      2.737364  0.073671  37.156  <0.01 ***
NA - IndoMalay__Mainland == 0                    -1.146172  0.061292 -18.700  <0.01 ***
Neartic__Island - IndoMalay__Mainland == 0       -0.701882  0.261997  -2.679  0.2544
Neartic__Mainland - IndoMalay__Mainland == 0      1.596890  0.068216  23.409  <0.01 ***
Neotropic__Island - IndoMalay__Mainland == 0     -0.784538  0.076736 -10.224  <0.01 ***
Neotropic__Mainland - IndoMalay__Mainland == 0   -0.359843  0.049988  -7.199  <0.01 ***
Oceania__Island - IndoMalay__Mainland == 0       -0.201449  0.183367  -1.099  0.9982
Oceania__Mainland - IndoMalay__Mainland == 0      0.145355  0.662907   0.219  1.0000
Paleartic__Island - IndoMalay__Mainland == 0      1.424923  0.166638   8.551  <0.01 ***
Paleartic__Mainland - IndoMalay__Mainland == 0    1.255223  0.057838  21.702  <0.01 ***
Neartic__Island - NA == 0                         0.444290  0.263934   1.683  0.9101
Neartic__Mainland - NA == 0                       2.743062  0.075778  36.199  <0.01 ***
Neotropic__Island - NA == 0                       0.361634  0.082680   4.374  <0.01 **
Neotropic__Mainland - NA == 0                     0.786329  0.059111  13.303  <0.01 ***
Oceania__Island - NA == 0                         0.944723  0.187579   5.036  <0.01 ***
Oceania__Mainland - NA == 0                       1.291527  0.664313   1.944  0.7757
Paleartic__Island - NA == 0                       2.571095  0.170614  15.070  <0.01 ***
Paleartic__Mainland - NA == 0                     2.401395  0.069207  34.699  <0.01 ***
Neartic__Mainland - Neartic__Island == 0          2.298772  0.260578   8.822  <0.01 ***
Neotropic__Island - Neartic__Island == 0         -0.082656  0.265558  -0.311  1.0000
Neotropic__Mainland - Neartic__Island == 0        0.342040  0.259416   1.318  0.9884
Oceania__Island - Neartic__Island == 0            0.500433  0.315880   1.584  0.9437
Oceania__Mainland - Neartic__Island == 0          0.847237  0.711572   1.191  0.9958
Paleartic__Island - Neartic__Island == 0          2.126805  0.306085   6.948  <0.01 ***
Paleartic__Mainland - Neartic__Island == 0        1.957105  0.263487   7.428  <0.01 ***
Neotropic__Island - Neartic__Mainland == 0       -2.381428  0.083371 -28.564  <0.01 ***
Neotropic__Mainland - Neartic__Mainland == 0     -1.956733  0.060481 -32.353  <0.01 ***
Oceania__Island - Neartic__Mainland == 0         -1.798339  0.190078  -9.461  <0.01 ***
Oceania__Mainland - Neartic__Mainland == 0       -1.451535  0.665066  -2.183  0.6044
Paleartic__Island - Neartic__Mainland == 0       -0.171967  0.172218  -0.999  0.9994
Paleartic__Mainland - Neartic__Mainland == 0     -0.341667  0.072978  -4.682  <0.01 ***
Neotropic__Mainland - Neotropic__Island == 0      0.424696  0.066504   6.386  <0.01 ***
Oceania__Island - Neotropic__Island == 0          0.583089  0.192659   3.027  0.1077
Oceania__Mainland - Neotropic__Island == 0        0.929893  0.665872   1.397  0.9805
Paleartic__Island - Neotropic__Island == 0        2.209461  0.175896  12.561  <0.01 ***
Paleartic__Mainland - Neotropic__Island == 0      2.039761  0.081406  25.057  <0.01 ***
Oceania__Island - Neotropic__Mainland == 0        0.158394  0.184289   0.859  0.9999
Oceania__Mainland - Neotropic__Mainland == 0      0.505197  0.663403   0.762  1.0000
Paleartic__Island - Neotropic__Mainland == 0      1.784765  0.166060  10.748  <0.01 ***
Paleartic__Mainland - Neotropic__Mainland == 0    1.615065  0.057176  28.247  <0.01 ***
Oceania__Mainland - Oceania__Island == 0          0.346804  0.685881   0.506  1.0000
Paleartic__Island - Oceania__Island == 0          1.626371  0.242903   6.696  <0.01 ***
Paleartic__Mainland - Oceania__Island == 0        1.456671  0.186456   7.812  <0.01 ***
Paleartic__Island - Oceania__Mainland == 0        1.279568  0.682040   1.876  0.8175
Paleartic__Mainland - Oceania__Mainland == 0      1.109868  0.663772   1.672  0.9151
Paleartic__Mainland - Paleartic__Island == 0     -0.169700  0.164396  -1.032  0.9991
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)
```

S3. Output of GLMM on all Covariables

S3.1. Island-restricted reptiles

Summary table

```
Generalized linear mixed model fit by maximum likelihood (Laplace
Approximation) ['glmerMod']
 Family: Negative Binomial(1)  ( log )
Formula: Npapers1stApproach ~ LogElevation + LogRangeRarity + StdYear +
LogBodyMass + LogNumBioInst + LogRangeSize + IUCN + (1 |
    Family)
   Data: dataset_ONI

     AIC      BIC   logLik deviance df.resid
  2840.9   2889.9  -1410.4   2820.9      981

Scaled residuals:
    Min      1Q  Median      3Q     Max
-0.9781 -0.6172 -0.4545  0.3478 12.0140

Random effects:
 Groups Name          Variance Std.Dev.
 Family (Intercept) 0.3051   0.5523
Number of obs: 991, groups:  Family, 49

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    0.25980    0.14367   1.808 0.070557 .
LogElevation  -0.07293    0.04535  -1.608 0.107809
LogRangeRarity -0.33271   0.07172  -4.639 3.50e-06 ***
StdYear       -0.45530    0.05923  -7.686 1.51e-14 ***
LogBodyMass    0.60824    0.06179   9.844  < 2e-16 ***
LogNumBioInst  0.36411    0.10001   3.641 0.000272 ***
LogRangeSize  -0.33053    0.13982  -2.364 0.018079 *
IUCN          -0.29275    0.05532  -5.292 1.21e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
           (Intr) LgElvt LgRngR StdYer LgBdyM LgNmBI LgRngS
LogElevatin  0.078
LogRangRrty -0.112 -0.251
StdYear      0.152 -0.126 -0.022
LogBodyMass -0.263  0.038  0.189  0.104
LogNumBInst  0.104 -0.191 -0.082  0.108  0.037
LogRangeSiz  0.295 -0.364  0.514  0.207 -0.073 -0.357
IUCN         0.028 -0.051  0.120  0.049  0.104  0.130 -0.083
```
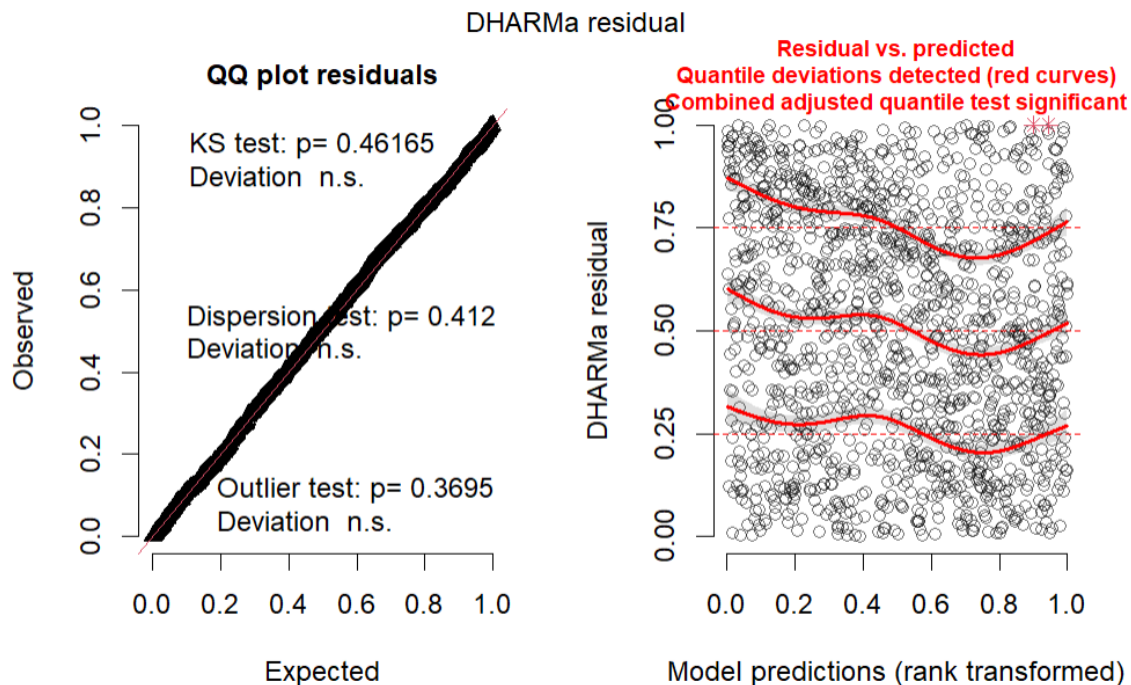
Residuals

Dredge output

```
Global model call: glmer(formula = Npapers1stApproach ~ LogElevation +
LogRangeRarity +
    StdYear + LogBodyMass + LogNumBioInst + LogRangeSize + IUCN +
    (1 | Family), data = dataset_ONI, family = negative.binomial(theta =
1),
    na.action = na.fail)
---
Model selection table
    (Intrc)   IUCN  LgBdM    LgElv  LgNBI   LgRnR    LgRnS   StdYr df    logLik   AICc   delta weight
127  0.2261         0.6195 -0.07807 0.3611 -0.2477 -0.33160 -0.4553  9 -2021.597 4061.3   0.00  0.536
128  0.2200 0.04812 0.6201 -0.07906 0.3555 -0.2489 -0.31830 -0.4567 10 -2021.042 4062.2   0.92  0.339
124  0.2405 0.04582 0.6297                  0.3264 -0.2794 -0.40530 -0.4684  9 -2023.207 4064.5   3.22  0.107
96   0.3109 0.06253 0.6119 -0.11890 0.2754 -0.1657          -0.4253  9 -2025.017 4068.2   6.84  0.018
112  0.1559 0.04443 0.6571 -0.12020 0.3272          -0.07443 -0.4556  9 -2030.149 4078.4  17.11  0.000
120  0.1525 0.06062 0.6225 -0.05061         -0.2274 -0.14880 -0.4785  9 -2030.402 4078.9  17.61  0.000
64   0.3534 0.03839 0.7009 -0.11950 0.4399 -0.2377 -0.07134          9 -2065.910 4149.9  88.63  0.000
126  0.5917 0.04202        -0.11410 0.3426 -0.3241 -0.23240 -0.5457  9 -2088.059 4194.2 132.93  0.000
Models ranked by AICc(x)
Random terms (all models):
  1 | Family
```

S3.2. Mainland reptiles

Summary table

```
Generalized linear mixed model fit by maximum likelihood (Laplace
Approximation) ['glmerMod']
 Family: Negative Binomial(1)  ( log )
Formula: Npapers1stApproach ~ LogElevation + LogRangeRarity + StdYear +
LogBodyMass + LogNumBioInst + LogRangeSize + IUCN + (1 |
    Family)
   Data: dataset_OFFI

     AIC      BIC   logLik deviance df.resid
  4981.4   5034.1  -2480.7   4961.4     1430

Scaled residuals:
    Min      1Q  Median      3Q     Max
-0.9702 -0.6324 -0.4327  0.3961  8.1479

Random effects:
 Groups Name           Variance Std.Dev.
 Family (Intercept) 0.5105   0.7145
Number of obs: 1440, groups:  Family, 69

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    0.67979    0.11964   5.682 1.33e-08 ***
LogElevation  -0.11105    0.05359  -2.072   0.0383 *
LogRangeRarity -0.35404    0.05867  -6.034 1.60e-09 ***
StdYear       -0.24170    0.05236  -4.616 3.91e-06 ***
LogBodyMass    0.53719    0.05732   9.372  < 2e-16 ***
LogNumBioInst  0.46968    0.06322   7.430 1.09e-13 ***
LogRangeSize   0.03030    0.09561   0.317   0.7513
IUCN          -0.27906    0.04207  -6.633 3.30e-11 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
           (Intr) LgElvt LgRngR StdYer LgBdyM LgNmBI LgRngS
LogElevatin -0.127
LogRangRrty  0.083 -0.120
StdYear     -0.015 -0.063  0.054
LogBodyMass -0.266 -0.003  0.018  0.120
LogNumBInst -0.136  0.067 -0.252  0.269 -0.020
LogRangeSiz  0.206 -0.149  0.606  0.251 -0.151 -0.529
IUCN        -0.016 -0.047 -0.107  0.102  0.098  0.126 -0.136
```
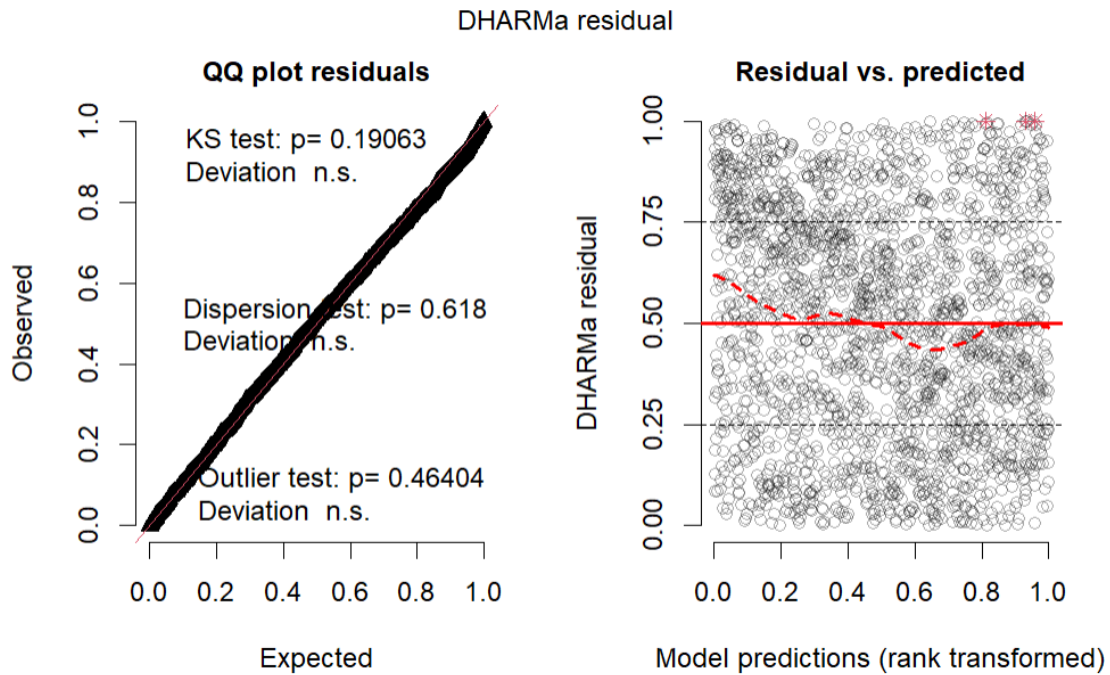
Residuals

DHARMa residual

QQ plot residuals

KS test: p= 0.19063
Deviation n.s.

Dispersion test: p= 0.618
Deviation n.s.

Outlier test: p= 0.46404
Deviation n.s.

Observed / Expected

Residual vs. predicted

DHARMa residual / Model predictions (rank transformed)

Dredge output

```
Global model call: glmer(formula = Npapers1stApproach ~ LogElevation + Log
RangeRarity +
    StdYear + LogBodyMass + LogNumBioInst + LogRangeSize + IUCN +
    (1 | Family), data = dataset_OFFI, family = negative.binomial(theta =
1),
    na.action = na.fail)
---
Model selection table
    (Intrc)    IUCN  LgBdM   LgElv   LgNBI   LgRnR    LgRnS   StdYr df    logLik   AICc  delta weight
124  0.6334 -0.09447 0.4972                 0.3760 -0.5560 -0.14450 -0.5076  9 -4136.403 8290.9   0.00  0.421
128  0.6534 -0.09756 0.4937 -0.05934 0.3662 -0.5483 -0.13130 -0.5112 10 -4135.551 8291.2   0.32  0.359
96   0.6843 -0.08915 0.4814 -0.07036 0.3181 -0.5031                 -0.4930  9 -4137.136 8292.4   1.47  0.202
127  0.6444          0.4963 -0.05041 0.3575 -0.5524 -0.10320 -0.5191  9 -4139.558 8297.2   6.31  0.018
120  0.7372 -0.07943 0.5254 -0.11240        -0.4650  0.17910 -0.5596  9 -4164.236 8346.6  55.67  0.000
126  0.9193 -0.10780        -0.08798 0.4020 -0.5493 -0.04346 -0.5269  9 -4184.738 8387.6  96.67  0.000
112  0.7648 -0.10770 0.4912 -0.13000 0.2268          0.35650 -0.5511  9 -4205.352 8428.8 137.90  0.000
64   0.6416 -0.13760 0.5222 -0.01948 0.4750 -0.5924  0.14240          9 -4229.114 8476.3 185.42  0.000
Models ranked by AICc(x)
Random terms (all models):
  1 | Family
```

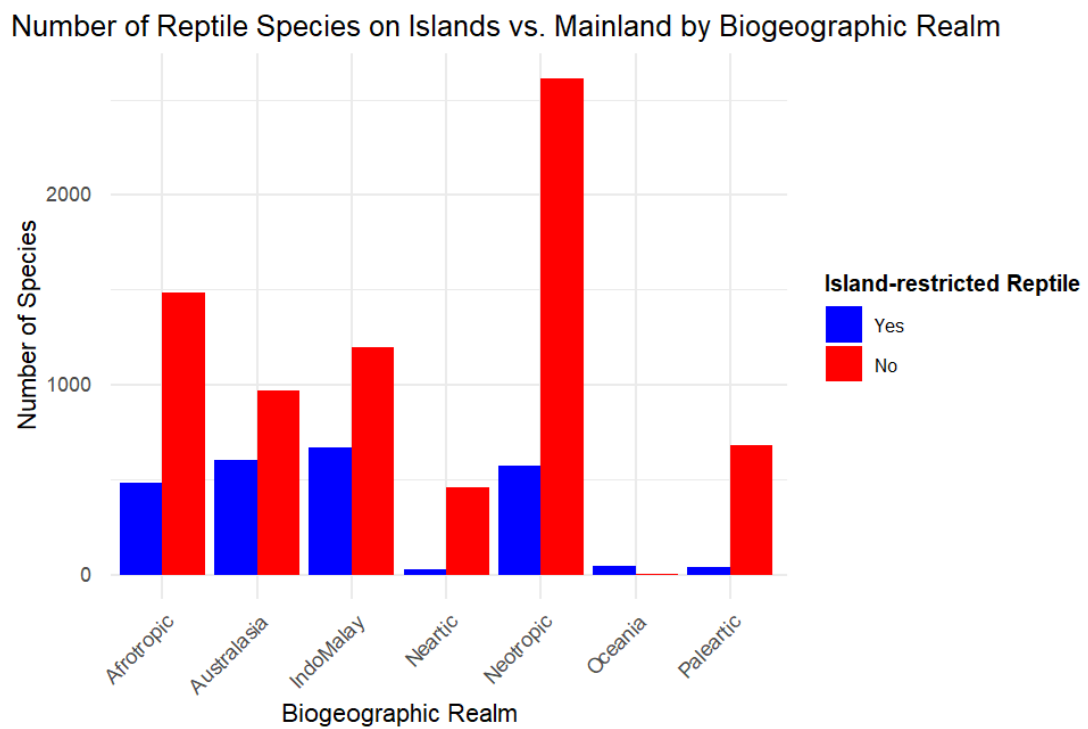## S4. Total reptile species found in each region

Figure S4: The total number of Island-restricted and mainland
species found in each realm.

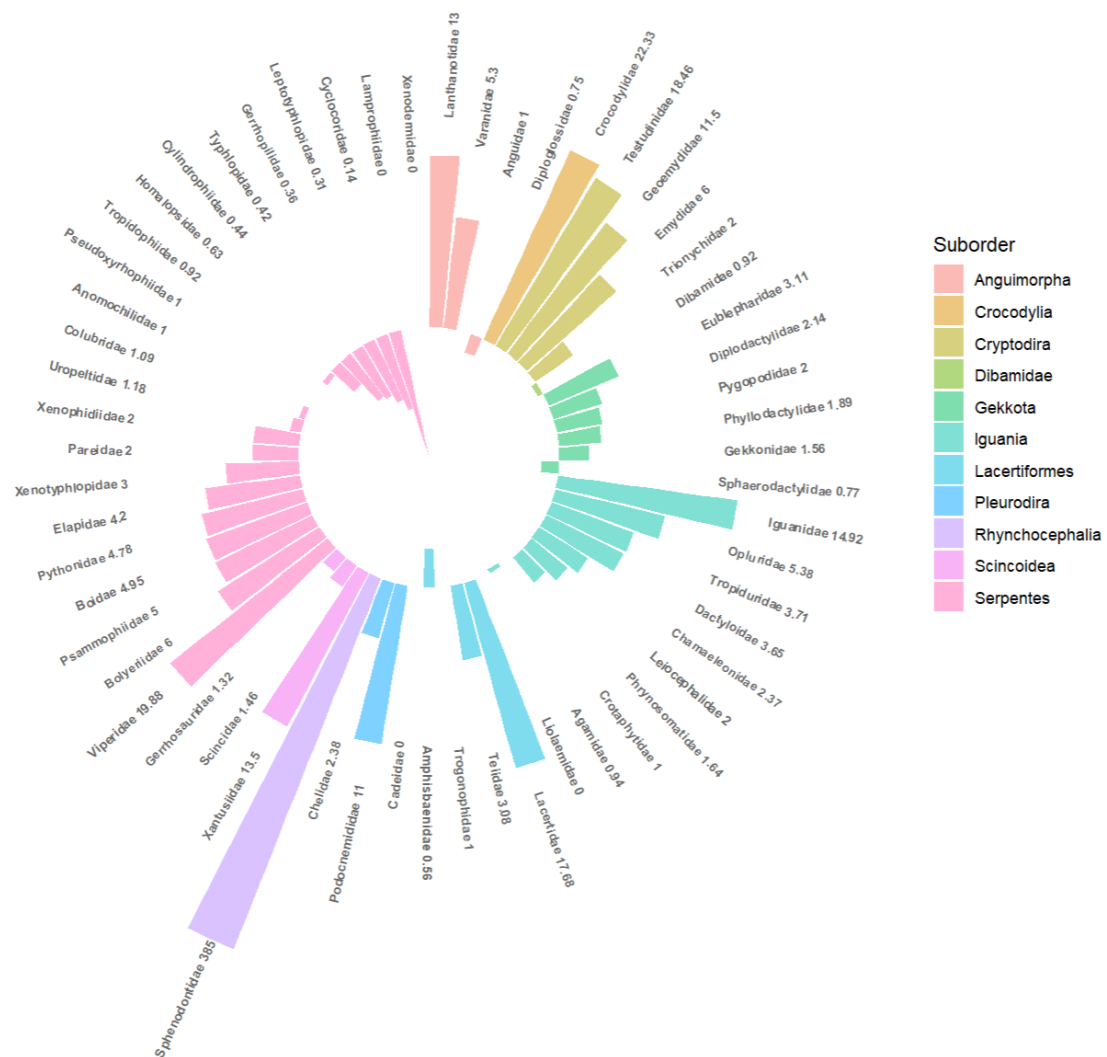# S5. The average research output of island-restricted reptile families

Figure S5: The mean research output of island-restricted members of
the different reptile families, colour coded by suborder.

Raw data and code

DrosophilaEnjoyer/Factors-affecting-reptile-research: The raw data
for my masters thesis and the code I used to analyse it (github.com)